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130
                                                                                    140
                                                                                                                      150
                                                                                                                                                         160
   1093 GGGGAAACCCAGCACGAGTGATGTCGTGCTACCCGCATCT M.tuberculosis
                 GGGGAAACCCAGCACGAGTGATGTCGTCGTACCCGCATDT
GGGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT
GGGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT
GGGGGAACCCACCACGAGTGATGTCGTGTACCCAACGCT
M.phlei
M.paratuberc.
GGGGAAACCCAACCACGAGTAATGTCGTGTTACCCGTATCT
M.phlei
M.gastri
GGGGAAACCCAGCACGAGTAATGTCGTGTTACCCGTATCT
M.kansasii
GGGGAAACCCAGCACGAGTGATGTCGTGTTACCCGCATCT
M.kansasii
   432
  2588 GGGGAAACCCGGCACGAGTGATGTCGTGTCACCAGGCGCT M.smegmatis
                                               210
                                                                                  220
                                                                                                                     230
                                                                                                                                                       240
  1172 CATCTCAGTACCCGTAGGAGGAGAAACAATTGTGATTCC M.tuberculosis
CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.tuberculosi
CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.avium
CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.paratuberc.
CATCTCAGTACCCGTAGAAAACAATTGTGATTCC M.phlei
CATCTCAGTACCCGTAGGAGAAAAACAATTGTGATTCC M.leprae
CATCTCAGTACCCGTAGGAGAAAACAAAAGTGATTCC M.gastri
CATCTCAGTACCCGTAGGAGAAAAAAAAAAAGTGATTCC M.kansasii
CATCTCAGTACCCGTAGGAGAAAAAAAAAAATTGTGATTCC M.smegmatis
                                              330
                                                                                 340
                                                                                                                    350
                                                                                                                                                      360
TGTGGGATGGTATGTCTCAGCGCTACCGGCTGAGA-GG M.tuberculosis
TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG M.avium
TGTGGGATTGATATGTCTCAGCTCTACCTGGCTGAGG-GG M.paratuberc.
TGTGGGATTGATATGTCTCAGCTCTGCCGCCGCGATGGCAG M.phlei
TGTGGGATTGGTATGTCTCAACTCTACCTGGTTCAGG-GG M.leprae
TGTGGGATTGGTATGTCTCAGCTCTACCGGCTGAGG-GG M.gastri
TGTGGGATCGATACGTCTACCGGCTGAGG-GG M.kansasii
TGTGGGACCTATCTTTCCGCCTCTACCTGGCTGAGG-GG M.smegmatis
```

Figure 1A

					-
	;	370	380	390 40	10
1327	AGTCAGA	AGTGTCGT	GTTAGCGGA	GTGGCCTGGGAT	M.tuberculosis
656	TAGTCAGA	AGTGTCGT	GGTTAGCGGA	AGTGGCCTGGGAF	M avium
656	TAGTCAGAZ	AG <u>TGTC</u> GT	ggttag <u>cg</u> ga <i>i</i>	GTGGCCTGGGA	M.paratuberc.
742	TAGTGATIA	vag <u>ca</u> gigit	ggttag <b>gt</b> ga <i>i</i>	GTGGCCTGGGAT	M.phlei
668	[]AGTCAGA	vagtg cgt(	<b>GTTAGCGGA</b>	ATGGCCTGGGAT	' M lenrae
443	CAGTCAGA	<b>VAGTGTCGT</b> (	ggtta <b>a</b> cggai	GTGGCCTGGGAT	' M.gastri
386	CAGTCAGA	VAGTGTCGT	GGTTAACGGA	GTGGCCTGGGAT	M kanangii
2823	CAGTGAGA	VAPTGTEGT(	GTTAGCGGA	<b>ATGGCTTGGGAT</b>	M.smegmatis
				-	
		150	460	470	•
				470 48	•
1406	CGGCACCTG	CCTAGTATO	CAATTCCCGAG	TAGCAGCGGGCC	M.tuberculosis
735	CGGCACCTG	CCTTATATO	CAACACCCGAG	TAGCAGCGGGCC	M.avium
735	CGGCACCTG	CCTPATATO	CAACACCCGAG	TAGCAGCGGGCC	M.paratuberc.
820		CITGTCACAC	∌G−⊣TCCCGAG	TAGCAGCGGGCC	: M.phlei
747 522	(I)GGCACCTG	CCTIGTATO	CAATTCCCGAG	TAGCAGCGGGCC	M.leprae
465	CGGCACCTG	CCTIGTATO	CAATTCCCGAG	TAGCAGCGGGCC	M.gastri
2902	CGGCACCTG	CCTIGTATO	CAATTCCCGAG	TAGCAGCGGCC	M.kansasii
2902	CGMCGTCTC	ELCTEGATEC	TGTTCCCGAG	TAGCAGCGGGCC	M.smegmatis
	-				
		190	500		•
			- : -	510 52	•
1446	CGTGGAATC	CGCTGTGA	ATCOSCCGGGA	CCACCCGGTAAG	M.tuberculosis
775	CGTGGAATC	TIGCTGTGA	TOTIGCCGGGA	CCACCCGGTAAG	M.avium
775	CGTGGAATC	IIGCTGTGA	ATCITGCCGGGA	CCACCCGGTAAG	M.paratuberc.
857	CGTGGAATC	TIGCTGTGA	TOTGCCGGGA	CCACCCGGTAAG	M.phlei
78 <b>7</b> 562	CGTGGAATC	TIGCTGTGA	TCIGCCGGA	CCACCCGGTAAG	M.leprae
505	CGTGGAATC	HECTGTGA	TOTGCCGGGA	CCACCCGGTAAG	M.gastri
2942	CGTGGAATC	HECTGTGA	ATCIGCCGGGA	CCACCCGGTAAG	M.kansasii
2942	CGTGGAATC	щестстская	ATOIIGCCGGGA	CCACCCGGTAAG	M.smegmatis

Figure 1B

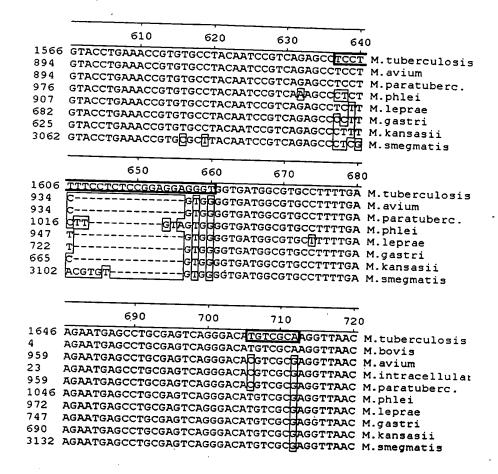


Figure 1C

		770	. 780	790	800	
1726	GACCC	ACACGCGC	ATACGCGCGTG	TCDDDDCDC		1.tuberculosis
84	CGACCC	ACACGCGC	ATACGCGCGTG	TGAATAGIGG	CGTGT	1.tuberculosis
1039	CGF	-CATGCGC	Trificion of	TGAATAGTGG	CGTGT N	1.bovis
103	cg	-cardedd	IIIIGGGGIGT	AGIGG	CGTGT N	1.avium
1039	ĊG	-Cardocr	TITGGGGTGT	AGTGG	CGTGT N	1.intracellula
1126	CGTATC	المجال والم	regerreere	AGTGG	CGTGT 1	1.paratuberc.
1052	CGTAT-		AGCGIGIGIE		GTGT 1	1.phlei
827	CGTAT-	-Cycecent	AGCGIGIGI	AGTGG	CGTGT N	1.leprae
770	CGTAT-	CACGCGII	MGCGIGIGI	AGTGG	CGTGT N	1.gastri
3212		COCOCOC	ACCOTOTOT	HDGTGG	COTOT N	4
3212	CGIAT	CCACACA	GAGTGTGTGG	TGTAGTGG	GTGT N	.smegmatis
					_	3
				-		
		970	980	990		
1006	10000	- : -			1000	
1926	ATTTAGG	TGCAGCGT	TGCGTGGTTC	ACCGCGGAGG'	TAGAG M	.tuberculosis
1220	~**********	1 L LTC - MITC 11 - 1	"""" - ( "" - "" - "" - "" - "" - "" -	1 CCMCCC		
1220	ALLINGG	TGCAGCGT	"ሆĠርርምርርጥተር፣	ひししかししょうかんしゅ		
1244	ATTTAGG	TGCAGCGT	TGCGTGGTTC:	ACCACGGAGGT	TAGAG M	lenrae
1019	ATTTAGG	TGCAGCGT	TGCGTĠĤTTC	ACCACGGAGGT	DEAG M	.reprae
	777700	TOCHECET	1140.1477471777777			
3408	ATTTAGG	TGCAGCGT	Gc-Archite	TEOCGEAGE	TAGAG M	. Kansasii
			Q Q V	<u></u> 000A001	AGAG M	.smegmatis
		1050	1060		<del></del>	
				1070	1080	
2005	CAGCCAA	ACTCCGAA	TGCCG-TGGTG	TA-AAGCGT	GGCA M.	tuberculosis
1307	CAGCCAA	ACTCCGAA	TGCCG-TGGTG	- תאשא אוריכית	GGCD M	arri
130/	CAGCCAA	ACTCCGDD	からししに 一かららから			
1401	CAGCCAA	ACTCCGAA	IGCCGATAAG-	ー かいかか かんかんか	GGCD M	nhlai
1323	CAGCCAA	ACTCCGAA	TGCCG-TGGTh		GGCD M	lannes
1030	CAGCCAA	ACTCCGAA'	TGCCG-TGGTG		GGCD M	~ ~ ~ ~ · · ·
1041	CAGCCAA	MCICCGAA	TGCCG-TGGTG		CCCD M	kanaaaii
3486	CAGCCAA	ACTCCGAA	rgccggraag		cook M.	Kansasii
				CALCALOTTOP	hadhwww.	smegmat13

Figure 1D

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1130
                                                                 1140
                                                                                             1150
                                                                                                                       1160
 2082 ACAGCCCAGATCGCCGGCTAAGGCCCCCAAGCGTGTGCTA M.tuberculosis
 1385 ACAGCCCAGATCGCCGGCTAAGGCCCCTAAGCGTGTGCTA M.avium
1385 ACAGCCCAGATCGCCGGCTAAGGCCCCTAAGCGTGTGCTA M.paratuberc.
 1479 ACAGCCCAGATCGCCGGCTAAGGCCCCTAAGCGTGTGCTA M.phlei
1401 ACAGCCCAGATCGCCGGCTAAGGCCCCTAAGCGTGTGCTA M.leprae
1175 ACAGCCCAGATCGCCGGCTAAGGCCCCAAAGCGTGTGCTA M.gastri
1118 ACAGCCCAGATCGCCGGCTAAGGCCCCAAAGCGTGTGCTA M.kansasii
3566 ACAGCCCAGATCGCCGGTTAAGGCCCCTAAGCGTTTGTTA M.smegmatis
                                   ,1290
                                                                1300
                                                                                            1310
                                                                                                                       1320
 2241 CTCAAGCACACCGCCGAAGCCGCGCACATCCACCTTGT- M.tuberculosis
1544 CTCAAGCACACCGCCGAAGCCGCGCACATTCATCTT TA M.avium
1544 CTCAAGCACACCGCCGAAGCCGCGCACATTCATCTT TA M.paratuberc.
1638 CTCAAGCACACCGCGGAAGCCGCGGGCA - ATCAGCGTTTT M.phlei
 1560 CTCAAGCACAGCGCGAAGCCGCGCACATTICACCTTOTA M.leprae
1334 CTCAAGCACACCGCGAAGCCGCGACA----ACCGC--A M.gastri
1277 CTCAAGCACACCGCCGAAGCCGCGACA----ACCGC--A M.kansas
                                                                                                                               M.kansasii
 3726 TTCAAGCACACCGCCGAAGCCGCGGAA--GCCAACGTTTG M.smegmatis
                                    1330
                                                               1340
                                                                                           1350
                                                                                                                      1360
 2280 -GGTGGGTGTGGGTAGGGGAGCGTCCCTCATTCAGCGAAG M.tuberculosis
2280 -GGTGGTGFGGGTAGGGGAGCGTCCCTCATTCAGCGAAG M.tuberculosi
1583 CGGTGGTGTGGGTAGGGGAGCGTCCCCCATTCAGCGAAG M.avium
1583 CGGTGGTGTGGGTAGGGGAGCGTCCCCCATTCAGCGAAG M.paratuberc.
1676 IGGCTGGTGTGGGTAGGGGAGCGTCCTGCATCGGGAAG M.phlei
1600 GGGTGGTTGGGTAGGGGAGCGTCCTCATTCAGCGAAG M.leprae
1367 AGGT----TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG M.gastri
1310 AGGT----TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG M.kansasii
1764 IT-----TGGGTAGGGGAGCGTCCTG-ATGCGGTGAAG M.smegmatis
```

Figure 1E

	<del></del>		<del></del>	<del></del>
	1370	1380	1390	1400
2319	CCACCGGGTGACCG	GTGGTGGAGGG	TGGGGGAGT	GAGAAT M.tuberculosis
1623	CT-CCGGGTGACCG	GTGGTGGAGGG	TGGGGGAGT	GAGAAT M.avium
1623	ch-ccg-ggtgaffice	GTGGTGGAGGG	TGGGGGAGT	GAGAAT M.paratuberc.
1716	CCCCEAGTGATIC	GTGGTGGAGGG	TGTGGGAGT	GAGAAT M phlei
1640	CCTCCGGTAACCG	GTGGTGGAGGG	TGGGGAAGT	GAGAAT M.leprae
1402	CCGCCGGGTGACCG	GTGGTGGAGGA	TGGGGGAGT	GAGAAT M.gastri
1345	CFGCCGGGTGACCG	GTGGTGGAGGA	TGGGGGAGT	GAGAAT M.kansasii
3796	CCCCCEAGTATICGE	ородория при	тепсескат	GAGAAT M.smegmatis
	4 4 6 4 4 6 1 1 1 1 1 1 1 1	Jo 1 0 0 1 0 0 A 0 0 0	TOEDGGAGT.	sadari M. smegmaciş
	1410	1420	1430	1440
2359	GCAGGCATGAGTAG	CGACAAGGCAA	GTGAGAACC	TTGCCC M.tuberculosis
1662	GCAGGCATGAGTAG	CGAMAAGGCAA	GTGAGAACC'	TTGCCC M.avium
1662	GCAGGCATGAGTAG	cgahaaggcaa	GTGAGAACC'	TTGCCC M.paratuberc.
1756	GCAGGCATGAGTAG	CGAHAAGGCAA	GTGAGAACC'	TTMCCC M.phlei
1680	GCAGGCATGAGTAC	CGATAAGGCAA	GTGAGAACC'	TTGCCC M.leprae
1442	GCAGGCATGAGTAG	CGAHAAGGCAA	GTGAGAACC	TTGCCC M.gastri
1385	GCAGGCATGAGTAC	CGAHAAGGCAA	GTGAGAACC'	TTGCCC M.kansasii
3836	GCAGGCATGAGTAG	CGALTAGGCAA	GTGAGAACC'	TTOCCC M.smegmatis
				<b>3</b>
				•
			•	
	1570	1580	1590	1600
2519				AAACCG M.tuberculosis
1821				AAACCG M.avium
1821				AAACCG M.paratuberc.
1915	CGIICCOTGAIGAA	CTCATTOTGCT	'AACCACCCA	AAAC에 M.phlei
1840	CGCCCGTGATGAA	rca-gcggtact	BACCACCCA:	AAACCG M.leprae
1602	CGCCCGTGATGAA'	CA-GCGGTACT	'AACCACCCA	AAACCG M.gastri
1545	CGCCCGTGATGAA	rca-gcggtact	AACCACCA	AAACCG M.kansasii
3996	CGIICCHTGAIIGAA'	rca-gcggtact	'AACCATICCA	AAACCA M.smegmatis

Figure 1F

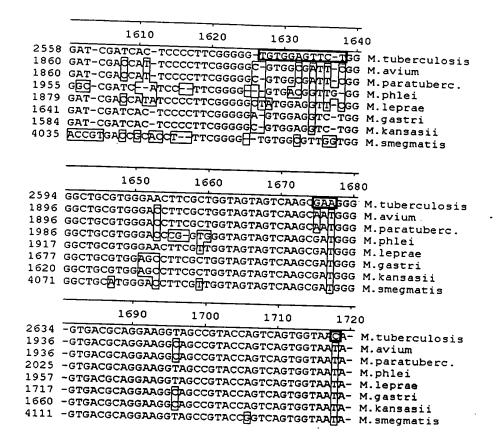


Figure 1G

	-		<del></del>	<del></del>	
	1730	1740	1750	1760	
2672	-CTGGGGCAAGCGG	TAGGGAGAG	GATAGGCAA	ATCCGT M.tuberculosis	
1974	-ctggggcaagcc	TAGE-AGAGO	CGATAGGCAA	ATCCGT M.avium	
				ATCCGT M.paratuberc.	
	-coggggggaaacchg				
1995	-CTGGAGCAAGCCDG	TAGGGAGAG	GATAGGCAN	ATCCGT M.lenrae	
1755	-CTGGGGCAAGCCAG	TAGGGAGAG	CGATAGGCAA	ATCCGT M.gastri	
1698	-CTGGGGCAAGCCAG	TAGGGAGAG	CGATAGGCAA	ATCCGT M.kansasii	
4149	-cligglighaagcchig	TAGGGAGTC	GATAGGIIAA	ATCCGT M.smegmatis	
				<b>,</b>	
	1970	1980	1990	2000	
				GGGAGC M.tuberculosis	
2208	AGGGGGCCGGAATA	OCGTGAACA	CCCTTGCGGT	GGGAGC M.avium	
				GGGAGC M.paratuberc.	
	AGGGGGACCCACGT				
	AGGGGGGCCGGAAT?	ATCGTGAACA	CCCTTGCGGT		
1910				M.gastri	
				GGGAGC M.kansasii	
4385	AGGGGGACCCACAT	GCGTGIIAAG	cclille	CCAAGC M.smegmatis	
			· · · · · · · · · · · · · · · · · · ·	<del></del>	
	2410	2420	2430	2440	
3345	ACCTCGACGCCAGTT	GGGGGGGAGT	CGTTGTTGAA	ATACC M.tuberculosis	
284	ACCTCGACGCCAGTT	GGGGCGGAGT	CGTTGTTGAA	ATACC M.bovis	
2645		TGTGTGGAGT	CGTTGTTGAA	ATACC M.avium	
393	ATACAGACGCCAGTT	TGTATGGAGT	CGTTGTTGAA	ATACC M.intracellulare	
2645	GCACAGACGCCAGTT	ngngnggag1	CGTTGTTGAA	ATACC M.paratuberc.	
2737	GCTCGGACGCCAGTT	GGGTGGAGT	CGTTGTTGAP	ATACC M.phlei	
2668	ACTITCGACGCTAGTT	GGGGIGGAGT	CGTTGTTGAP	ATACC M.leprae	
1910		<del>-</del> .		M.gastri	
2372	ACCTCAACGCCAGTT	GGGGTGGAGT	CGTTGTTGAF	ATACC M.kansasii	
4822	GCTCACACGCCAGTG	TGGGTGGAGT	CGTTGT <b>TGA</b>	AATACC M.smegmatis	

## Figure 1H

		· · · · · · · · · · · · · · · · · · ·			
		2450	2460	2470	2480
3385 7	ACTCTGA	TCGTATTG	GCATCTAAC	TCGAACCC	FGAATC M.tuberculosis
324 F	ACTCTGA	TCGTATTG	<b>GCATCTAAC</b>	CTCGAACCC	TGBBTC M howie
2685 <i>I</i>	ACTCTGA	TCGTATTG	SACACCTAAC	TCGAACCC	TETATO M avium
433 I	ACTCTGA	TCGTATTG	SACACCTAAC	TCGAACCC	TATC M.intracellula
2685 <i>I</i>	ACTCTGA	TCGTATTG	SACACCTAAC	TCGAACCC	THATC M paratubors
2111 7	<b>ACTCTGA</b>	TCGTATTG	<b>GCCTCTAAC</b>	TCGGACCG	redare M phisi
2708 7	ACTCTGA	TTGTATTG	AACATCTAACO	TCGAACCG	TATATC M.leprae
1910					M dagtri
2412 7	ACTCTGA	TCGTATTG	FACADCTAACE	TCGAACCC	TGARTC M kangagii
4862 F	ACTCTGA	TCGTATTG	GOOTCTAAC	TCGGACCG	TATATC M.smegmatis
					entrio in smegmacis
-			· · · · · · · · · · · · · · · · · · ·		<del></del>
		2490	2500	2510	2520
3425 7	GGTTTA	GEGACAGTO	SCCTGGCGGG	ים בתיידים בכי	GGGGC M.tuberculosis
364 0	GGGTTTA	GGGACAGT	CCTGGCGGG	יםמידים	regege M.bovis
2724	GGTTDA	DGGACAGTO	CCTGGCGGG	ים בייים אריי ים בייים אריים אריי	IGGGGC M.avium
472	GGTTCA	CGGACAGT	CCTGGCGGG	ים ביידים ברי	rggggc M.intracellula
2724	GGTTCA	CGGACAGT	CCTGGCGGG	ים ביים האת המיים את המיים המיים המיים המיים המ	rggggc M.Intracellula rggggc M.paratuberc.
2817 F	3GGTTTA	GGGACAGT	accreemeee		rededc M.paracuberc. regege M.phlei
2748	CGTTTA	GGGACAGT	CCTGGLGGG:	PAGITIAAC.	redecc m.phiei regece M.leprae
1910	3001111	00000000	3001990999	IAGITIAAC.	
	್ಡರ್ಗ್ಗೌಗ	Певасает	ברריים כרים ביי	בא המשפט א כי	M.gastri IGGGGC M.kansasii
4902 F	GGTTHA	GGGACAGI	CCTGGGGGG	PAGILIAAC,	redect M.kansasii redect M.smegmatis
	2001152	COGNONGIO	accido <u>li</u> dad.	INGITIANC.	redec M.smegmatis
					·
-		-			<del>_</del>
		2930	2940	2950	2960
864 7	AGTACGA	GAGGACCG	GGACGGACGA	ACCTCTGGT	GCACCA M.tuberculosi
3163 <i>I</i>	AGTACGA	GAGGACCG	GGACGGACGA	ACCTCTGGT	ATACCA M.avium
3163 7	AGTACGA	GAGGACCG	GGACGGACGA	ACCTCTGGT	ATACCA M.paratuberc.
3256 1	AGTACGA	GAGGACCG	GGACGGACGA	ACCTCTGGT	ATACCA M.phlei
3187 7	AGTACGA	GAGGACCG	GGACGGACGA	ACCTCTGGT	ATACCA M.leprae
910					M.gastri
		CBCCBCC	GENCERICEN	ಶ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧ ೧	GCACCA M.kansasii
2891 7	AG TACGA	GAGGAC! IT			

Figure 1I

		2970	2980	2990	3000	
390	4 GTTGT <u>CC</u>	CCGCCAGGG	GCACCGCTG	GATAGCCACGT	TCGOT M	cuberculosis
320:						uberculosis
320:	o Grigio	ノンドししんじじじ	GCACIGGCTG	こりひりつつつちつつゃ		avium
3296	o grigico	CACCAGGG	GCACCGCTG	ころかみらここれっこっ	maaabi '	paratuberc.
3221	7 GTTGTC	CACCAGGG	GCACCGCTG	GATAGCCACGT		hlei
1910	י כ		000000100	SATAGCCACGT		eprae
2931	l GTTGTCC	CDCCAGGG	Checama		_ M.g	astri .
5382	CTTGTCC	COCCACCA	SCACCGCTG(	GATAGC[[ACGT	TCGGA M.k	ansasii
0002	- 0110100	CHCCAGGG	3CACGGCTG	SATAGCEACGT	TCGGA M.s	megmatis
					_	
		3010	3020	2020		
2011				3030	3040	
3944	CAGGATA	accgctgap	AGCATCTAA	GCGGGAAACC	TTCTC M. +	uberculosis
2243	CAGGATA	ACCECTEAR	AGCATCTAA	CCCCCNNNCO	TROPO	O T CIT!
						aratuperc.
3267	CAAGATA	ACCGCTGAA	AGCATCTAA	GCGGGAAACC'		hlei
1910	_			CCCCCAAACC		eprae
2971	CAGGATA	ACCGCTGAA	AGCATCTAN	GCGGGAAACC'	м.д	astri
5422	CAGGATA	ACCGCTGDD	ACCRECES A	GCGGGAAACC' GCGGGAAACC'		
_		.00001074	AGCATCTAA	GCGGGAAACC	гсттс м.з	megmatis
						·
		<del></del>				
		3090	3100	3110	3120	
4023	CCCGC-AG	AACACGGG	TTCAATAGGT	CAGACCTGGA	AGCT M +	hammul
609	CCCGC-AG	MACACGGG	PTCAATAGGT	ירשהשררתההאי	ACCM M has	
3322	CCCGC-AG	AUCACGGG	ארוידות מוטידודות	***************		
677	CCCGC-AG	ACCACGGG	TTCCATAGGC	CREACCIGGA	AGCT M. AV	ıum
3322	CCCGC-AG	ATCACGGG		Charactega	AGCT M.in	tracellulare ratuberc.
3415	CCCGC-AG	ACACGGG	T-E-GA TAGGC	CAGACCTGGA CAGACCTGGA	AGCT M. par	ratuberc.
3309	- 2000 AG	. <del></del>	1. CEMINGHO	PAGACCTGDAK	JGCHHM.pn.	Le1
1910					M.lej	
3050	CCCGC-NO	חחרתרכים		laa aa aa a	M.gas	stri
5501	CCCGC-AG	AACACGGGT	TCGATAGGC	CAGACCTGGAI	AGCT M.kar	nsasii
J J O I	CCCGC-AG	ALCAUGGGF	YITGATAGAC	CAGACCTGGAZ	ACCOUNT AREA	

Figure 1J

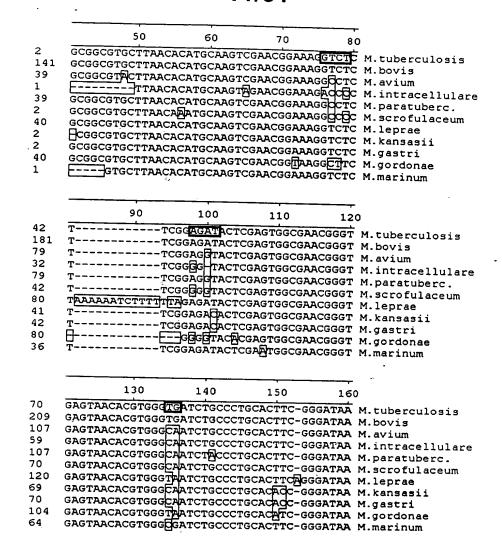


Figure 2A

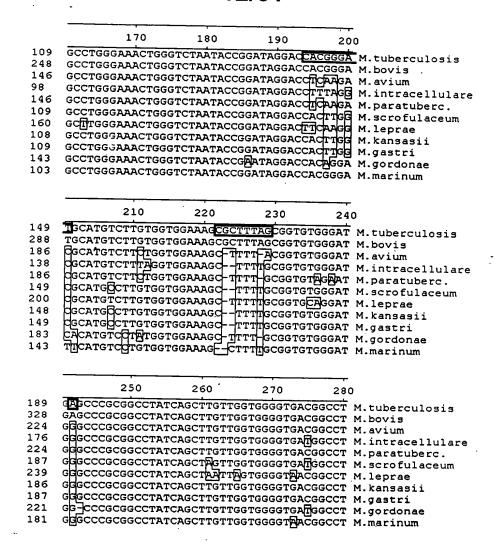


Figure 2B

	450	460	47	'0 48	0
389	AAACCTCTTTC	ACCATCGACG	ARGTCCGG	GTT CTCTCCC	M.tuberculosis
528	AAACCTCTTTC	ACCATCGACG	AAGGTCCGG	COMMENCE CICGG	M. tuberculosis
424	AAACCTCTTTC	ACCATCGACG	ABGGTCCGG	COMPRESSOR	M.DOV1S
376	AAACCTCTTTC	ACCATCGACG	ABGGTCCGG	COMMERCE	M.avium M.intracellulare
424	AAACCTCTTTC	ACCIATICGACG	DDGGTCCCC	CHIMPIONICA	
387	AAACCTCTTTC	ACCATCGACG	AACCTTCT.	erilitetage	M.paratuberc. M.scrofulaceum
439	AAACCTCTTTC	ACCATOGACE	AAGGTCTGG		M. scrotulaceum
386	AAACCTCTTTC	ACCATCGACG	ARGET CEC	CONCRETE	M.leprae
387	AAACCTCTTTC	ACCATCGACG	ARGETCCCG	GTTCTCTCGG	M. Kansasii
420	AAACCTCTTTC	ACCATCGACG	ARGETCCCC	CERTIFICACEG	M.gastri
381	AAACCTCTTTC	ACCATCGACG	AAGGTWCGG	CTTTTCTCGG	M.gordonae
			waa ilicaa	G1 IEITCTCEG	M.marinum
		<del></del>			
	1130	1140	115	0 116	0
1060	TCTCT TCTTCC				
1209	TCTCATGTTGC	CAGCACGTAA	TGGTGGGGA	CTCGTGAGAG	M.tuberculosis
1104	TCTCATGTTGC	CAGCACGTAA	TGGTGGGGA	CTCGTGAGAG	M.bovis
1056	TCTCATGTTGC	CAGCGGGTAA	TGCGGGGA	CTCGTGAGAG	M.avium
1000	TCTCATGTTGC	CAGCGGGTAA	TGCCGGGGA	CTCGTGAGAG	M.intracellulare
1098	TCTCATGTTGC	CAGCGGGTAA	TGCAGGGGA	CTCGTGAGAG	M.paratuberc.
1004	TUTCATGTTGC	CAGCGGGTAA'	TGCCGGGGA	CTCGTGTGTG	M. anna full and a
1113	TUTUATGTTGC	CAGCACGTAA'	ТССТССССЪ	CTCCTCACAC	M lanus
1000	TCTCATGTTGC	CAGCGGGTAA	rgcqgggga	CTCGTGAGAG	M.kansasii
11007	TCTCATGTTGC	CAGCGGGTAA'	recaeeey	CTCGTGAGAG	M.gastri
1000	TCTCATGTTGC	CAGCEGGTAA'	recdecer	CTCGTGAGAG	M.gordonae
1001	TCTCATGTTGC	CAGCACGTAA!	rggtgggga	CTCGTGAGAG	M.marinum
		· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	<del></del>	
	1250	1260	127	0 128	0
1189	CAATGGCCGGT	CAAAGGGCTC	CGATGCCG	CAGGTTAAG	M.tuberculosis
1328	CAATGGCCGGT	ACABAGGGCTO	ECGATGCCG	CARGUTAAG	M boris
1224	CAATGGCCGGT	ACAAAGGGCTC	CGATGCCG	DAGTTODAGT	M avium
1176	CAATGGCCGGT	ACAAAGGGCTO	CGATGCCG	PAGGTTARG	M.intracellulare
1210	CMMIGGCCGGI	ACAAAGGGCTC	CGATGCCG	דשמההתידשמה	M naratubers
1184	CAATGGCCGGT	ACAAAGGGCTC	CGATCCCC	PAGGTTARG	M scroful acaum
1239	CAATGGCCGGT	ACAAAGGGCT	CGATGCCG	DAGGTTAAG	M.scrofulaceum M.leprae
1186	CAATGGCCGGT	ACAAAGGGCT	CGATGCCG	CARGGTTAAG	M. kansasii
1187	CAATGGCCGGT	ACAAAGGGCTG	CGATGCCG	CGAGGTTAAG	M.gastri
1220	CAATGGCCGGT	ACAAAGGGCT	CGATGCCG	CGAGGTTAAG	M.gordonae
1181	CAATGGCCGGT	ACAAAGGGCT	CGATGCCG	CGAGGTTAAG	M.marinum

Figure 2C

culosis
cellulare
cellulare uberc. ulaceum
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Figure 2D

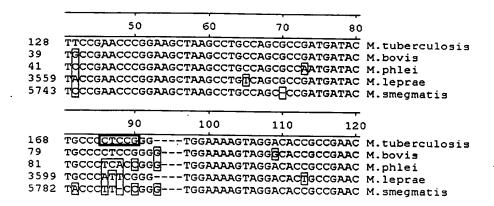


Figure 3

		<del></del>	<del></del>	<del></del>	
	90	100	110	120	
382	GGGAGCTGTCAA	CCGAGGATTGAT	CCGAGGATTT	CCGAAT M.avium	
382	COCCACTGICAN	CCGAGCATTGATG	ここことにことがこれ		
1053	GGGAGCTGTCAA	CCGAGCRTRGATA	$^{\circ}$	CCCDDG	
467	GGGAGCTGTCAA	CCGAGCITTIGGATG		CCCDDM W	. 3
392	GGGAGCTGTCAA	CCGAGCGTGGAT	CCGAGGATTT	CCGDDT M lamma	
167	GGGAGCTGTCAA	CCGAGCGTGGAT	CGAGGATTT	CCGDDT M manne	
110	GGGAGCTGTCAA	CCGAGCGTGGATC	CCAGGATTT	CCGDDE M lane	
2548	GGGAGCTGTCAA	CCGAGCGTTGATC	CGAGGATGT	CCGAAT M. Kansasii CCGAAT M. smegmatis	
		` _		oscient in smedmatis	
	<del></del>			· · · · · · · · · · · · · · · · · · ·	
	170	180	190	200	
462	GAATATATAGGG	GCG-GGAGGTA	CCCCCCC	GTGAAA M.avium	
462	GAATATATAGGG	MILDONOO OOO	CCCCCCC	GTGAAA M.avium GTGAAA M.paratuberc.	
1133	GAATATATAGGGT	rece-eeaeedan	CCCCCCC	GTGAAA M.paratuberc. GTGAAA M.tuberculosi	
547	GAATATATAGGCC		CCCCCCC	GTGAAA M.tuberculosi GTGAAA M.phlei	3
472	GAATATATAGGGT	11CG-GGD00 011C	CCCCCCAA	GTGAAA M.phlei GTGAAA M.leprae	
247	GAATATATAGGGT	ACCO-GGAGGGAA	CGCGGGGAA	GTGAAA M.leprae GTGAAA M.gastri	
190	GAATATATAGGGT	GCG-GGAGGGAA	CGCGGGGAA	GTGAAA M.gastri GTGAAA M.kansasii	
2628	GAATATATAGGCG	TCTT-GGGGGAA	AADDDDDDDD.	GTGAAA M.Kansasii GTGAAA M.smegmatis	
		To an Gooding	сосоодолл	FIGAAA M.SMegmatis	
				•	
				<del></del>	
	250	260	270	280	
541	-GTCAGTAGTGGC	GAGCGATC-CCC	DDCD COO	WARCE M. avium	
541	-GTCAGTAGTGGC	GAGCGAAC-CGG	<u>MACA-G</u> GCTA	WACCG M.avium WACCG M.paratuberc.	
1212	-GCAAGTAGTGGC	GAGCGAACECGG	NACA-GGCIP	MACCG M.paratuberc. MACCG M.tuberculosis	
626	-GTGAGTAGTGGC	GAGCGAAFAGGG		MACCO M. Tuberculosis	3
551	-GEAAGTAGTGGC	GAGCGAACGTCC		AACCG M.tuberculosis AACCG M.phlei AACCG M.leprae	
326	-GTCAGTAGTGGC	GAGCGAACGCGG		AACCG M.leprae AACCG M.gastri	
209	-GTMAGTAGTGGC	GAGCGAACGCGG:		BBCCG M kommonii	
2706	GTGAGTAGTGGC	GAGCGAACACCC	AEGATIGE CTA	AACEG M. Kansasii AACEG M. smegmatis	
			52 PO 00 12	www.b w. smedmat13	

Figure 4A

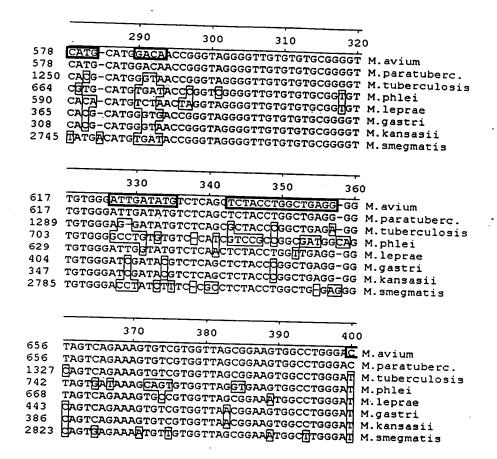


Figure 4B

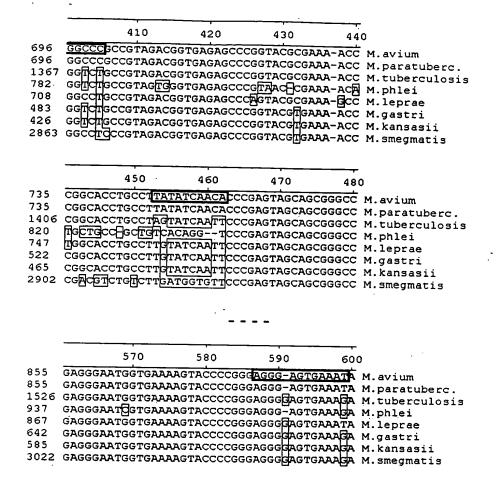


Figure 4C

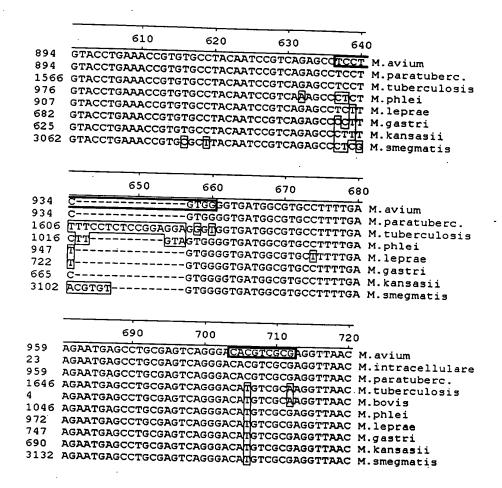


Figure 4D

		770	780	790	800
1039	CCCATCC	СТТТССС		G = G = G = G	• •
103	CGCATCC	CTTTGGG		GTGTAGTGGCG	TGT M.avium
1039		ज्ञाराउद्ध== ज्ञीराउद्ध===		GTGTAGTGGCG	TGT M.intracellulare
1726	CCECCO	TO CCCC CONTRA		GTGTAGTGGCG	TGT M.paratuberc.
84	CCACCAC	ACCOCATA	CUCULTAT	このカゲカでやっっっっ	mam 14
			<u>CG</u> CGCG1G1k	JAATAGTGGCG	TGT M hovis
1050		arcaran in	GGGGTTG	STGTAGTGGTG	TGT M.phlei
1032	CGHATCAC	e∏ere⊬ece	11(	STGTAGTGGCG	TGT M.leprae
827	CGITATCAC	CGTENCCG	11	TGTAGTGGCG'	TGT M.gastri
770	CGITATOGC	GCGCGAGCG	n	TGTAGTGGCG'	TGT M.kansasii
3212	CGITATCO	CACAAGAGT	GTGTG	TGTAGTGGTG	TGT M.smegmatis
					101 M.Smegmatis
				•	
		1050			<del></del>
		1050	1060	1070	1080
1307	CAGCCAAA	CTCCGAATG	CCG-TGGTG	-TAAAAGCTTG	GCA M.avium
~~~		IC I CCGAATTA	CCG-TGGTM.		
1098	CAGCCAAA	CTCCGAATC	CCG-TGCTE		GCA M.leprae GCA M.gastri
1041	CAGCCAAA	CTCCGAATG	CCG-TGGTG.	TATALGCGTG	GCA M.gastri G <u>C</u> A M.kansasii
3486	CAGCCAAA	CTCCCDAMC	cce-reere.	- TATAL GCGIG	GCA M.kansasii
	ON COCKAG	CICCGAATG	CCGGTAVGG	<u>COANGACII</u> CDC	GCA M.Kansasii GAA M.smegmatis
		•		-	
			<del>- ,</del>	<del> </del>	<del></del>
	1	L170	1180	1190	1200
1425	AGTGGAAA	AGGATGTGT	AGTCGCACA-	CACAACCAC	AGG M.avium
1425	AGTGGAAA	AGGATGTGT	GTCGCACA-	-GACAACCAGG,	AGG M.avium AGG M.paratuberc.
1519	AGTGGAAA	ACCATOTO		GACAACCAGG	AGG M.tuberculosis
1441	AGTGGAAA	ACCAMOMO TO TO	AG TOGO GAE	SACAACCAGG	AGG M.tuberculosis AGG M.phlei
1150	D CTCCCC 5	AGGATGTGO	AGTCGCAGA-	-GACAACCAGG	AGG M.1eprae AGG M.gastri AGG M.kansasii
1100	VOI GGGWW	AGGATGTGO	GTCGCAGA-	GACAACCAGG	AGG M.kansasii
2000	AGTGGAAA	AGGATGTGA	<b>AGTCGCAGA</b>	GAPAACCAGG:	AGG M.smegmatis
				_	-

### Figure 4E

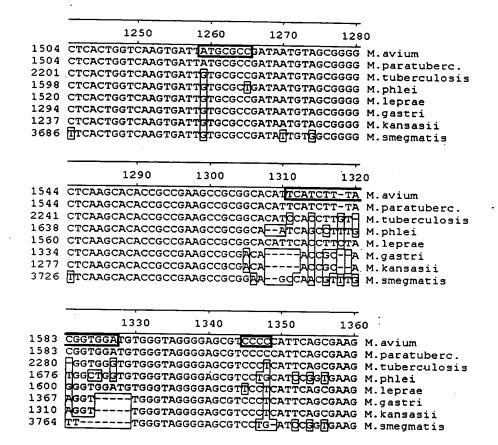


Figure 4F

		1370	4.4.4.	<del></del>	<del></del>
1.000			1380	1390	1400
2319 1716 1640 1402 1345	CTACCGGG CCGCCGGG CCGCCGGG	TGACCGGT TGACCGGT TGACCGGT TGACCGGT	GGTGGAGGGT GGTGGAGGGT GGTGGAGGGT GGTGGAGGAT GGTGGAGGAT	GGGGGAGTGA GGGGGGAGTGA G∏GGGAGTGA GGGGAGTGA	GAAT M.avium GAAT M.paratuberc. GAAT M.tuberculosis GAAT M.phlei GAAT M.leprae GAAT M.gastri GAAT M.kansasii GAAT M.smegmatis
				· <b>-</b> .	
	1	1530	1540	1550	1560
1781	CGATGGAC	AACGGGTT	ATATTCCCC		TGGG M.avium
1781	CGATGGAC	AACGGGTT	PATATTCCCG	TACCCGTGTA	
2479	CGATGGAC	AACGGGTT	SATATTCCCG	PACCEGTGTA	
10/5	CGATGGAC	AACGGGTT	ころつつつかではてほこ	77.000000	
1800	CGATGGAC	AACGGGTTC	ATATTCCCG	PACCEGTGTA	
1562	CGATGGAC	AACGGGTTC	SATATTCCCG	ACCCGTGTG	rene M.leprae
1505	CGATGGAC	AACGGGTTG	ATATTCCCG	ACCCGTGTG	
3956	CGATGGAC	AACGGGTTG	SATATTCCCG	ACCCGTGTG	
			ATATICCCG	ACCCGTGTA	GMG M.smegmatis
	1	.570	1580	1500	<del></del>
1021				1590	1600
1021	CGTCCCTG	ATGAATCA-	GCGGTACTA	CCACCCAAA	CCG M.avium
2510	cercetre,	ATGAATCA-	GCGGTACTA	CCACCCAAA	CCG M.avium
	~~~~~~	WOMAT CA-	Lillian Pacmaa	へんりんくくりょうかん	222
1040		ATGAATCA-	GCGGTACTHA	<b>ででなべてでなれれれ</b> れ	CCC N 1
1545		MIGAATCA-	GUGGTACTAA	.CCACCCAAAA	CCG M.Jeprae CCG M.gastri
3996	CGTCCDTG	AIGAATCA-	GCGGTACTAA	CCACCCAAAA	CCG M. kansasii
	oo room rea	AIGAATCA-	GCGGTACTAA	CCAIICCAAAA	CCA M. smegmatis

Figure 4G

	<del></del>					
	161	10 , 1	620 1	.630	1640	1
1860	GAT-CGACCA	<b>デーサーCCCT</b> 1	Cececer-c	TCCCCAMB (	<del></del>	
1860	GAT-CGACCA	T-TCCCCT		TCCCCARR (	100 i	M.avium M.paratuberc.
2558	GAT-CGAMCA	n-1000011	D- ⊃000000. ⊃R-⊒000000	TCCDCDDDC	- 00 i	M.paratuberc. M.tuberculosis
1955	GEG-CGATCE	- Purc CE-Tra	.ceeeee	TCDCCCCCCCC		M.tuberculosis
1879	GAT-CGACCA		Cececchi	remediate.	700 1	M.pniei
1641	GAT-CGACCA GAT-CGATICA	H-TCCCCT1	CGGGGGGTA	TCCDCCDC	-00 i	M. leprae
1584	GAT-CGATCA		ceeeeec-c	Techelone		M.gastri
4035	BCCGTGBCCG		9-2000001 2m			M.kansasii M.smegmatis
	rigoo Jorroop	<u> </u>		товсептве.	ני שטען	M.Smegmatis
					<del></del>	
	165				1680	
1896	GGCTGCGTGG	GACCTTCGC	TGGTAGTAG	TCAAGCAAT	GG 1	M.avium
1896	GGCTGCGTGG	GACCTTCGC	TGGTAGTAG	TCAAGC <u>AAT</u> 0	GG I	M.paratuberc.
2594	GGCTGCGTGG	GANCTICGO	TGGTAGTAG	TCAAGCGAA	GG I	M.tuberculosis
1986	GGCTGCGTGG	GACCCG-GI	GGGTAGTAG	TCAAGCGATO	GG I	M.tuberculosis M.phlei
1917	GGCTGCGTGG GGCTGCGTGG	GAACTTCG	TGGTAGTAG	TCAAGCGATO	GG 1	M.leprae
1677	GGCTGCGTGG	AGCCTTCGC	TGGTAGTAG	TCAAGCGATO	GG I	M.gastri
1620	GGCTGCGTGG	AGCCTTCGC	TGGTAGTAG	TCAAGCGATO	GG 1	M.kansasii
4071	GCTGCPTGG	GACCTTCG	TGGTAGTAG	TCAAGCGATO	GG I	M.smegmatis
		•				
	169	100	700 1	710	 1720	•
			-			•
1936	-GTGACGCAG	GAAGGCAGC	CGTACCAGT	CAGTGGTAA	1 -A1	M.avium
1936	-GTGACGCAG	GAAGGCAGC	CGTACCAGT	CAGTGGTAA	EA- I	M.paratuberc.
2634	-GTGACGCAG	GAAGGIJAGO	CGTACCAGT	Cagtggtaak	‡Α- Ι	M.tuberculosis
2025	-GTGACGCAG	GAAGGIJAGO	CGTACCAGT	CAGTGGTAA:	ra- I	M.phlei
1957	-GTGACGCAG	GAAGGIJAGC	CGTACCAGT	CAGTGGTAA	ra- I	M.leprae
1/1/	-GTGACGCAG	GAAGGCAGC	CGTACCAGT	CAGTGGTAA:	ra- I	M.gastri
1660	-GTGACGCAG	GAAGGCAGG	CGTACCAGT	CAGTGGTAA	ra- I	M.kansasii
4111	-GTGACGCAG	GAAGGIJAGC	CGTACCEGT	CAGTGGTAA	[A- ]	M.smegmatis
		<del></del>	<del>,</del>			
	173	30 1	740 1	.750 ·	1760	1
1974	-CTGGGGCAA	GCCCGTAG-	-AGAGCGAT	AGGCAAATC	GT 1	M.avium
1974	-CTGGGGCAA	GCCCGTAG-	-AGAGCGAT	AGGCAAATC	CGT I	M.paratuberc.
2672	-CTGGGGCAA	GCCGGTAGE	GAGAGCGAT	AGGCAAATC	CGT	M.tuberculosis
2063	-COGGGGTTAA	ACCHGTAGE	GGGAGTGAT	AGGCAAATC	CGT	M.phlei
1995	-CTGGAGCAA	GCCCGTAGE	тарурарды	AGGCAAATC	CT :	M lenrae
1755	-CTGGGGCAA	GCCAGTAG	GAGAGCGAT	AGGCAAATC	CGT 1	M.gastri
1698	-CTGGGGCAA	GCCAGTAG	GAGAGCGAT	AGGCAAATC	CGT	M.kansasii
4149	-cegeeeefiaa	.gcchgtagk	GAGTCAGAT	AGGITAAATC	CGT :	M.smegmatis
				_		

Figure 4H

```
1810
                                1820
                                             1830
                                                           1840
 2051 CG-AATTCGGTGATCCTCTGCTGCCAAGAAAGCCTCTA- M.avium
 2051 CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA- M.paratuberc.
 2751 CG-AATTCGGTGATCCTCTGCTGCCAAGAAAGCCTCTA- M.tuberculosis
 2141 сд-ааттсдатсстртдстепсвадаааадсстста- м.phlei
 2074 CG-AATTCGGTAAGCCTCTGCTGCCAAGAAAAGCCTCTA- M.leprae
 1834 CG-AATTCGGTGATCCTCTGCTGCCAAGAAAGCCTCTA- M.gastri
 1777 CG-AATTCGGTGATCCTCTGCTGCCAAGAAAAGCCTCTA- M. kansasii
 4228 CG-AATTCGGTGATCCTATGCTGCCGAGAAAAGCCTCTA- M.smegmatis
                 1850
                               1860
                                             1870
                                                          1880
2089 GCGAGCACATACA CGGCCCGTACCCCAAACCAACACAGGT M. avium
2089 GCGAGCACATACACTGCCCGTACCCCAAACCAACACAGGT M.paratuberc.
2789 GCGAGCACAGACCGGCCCGTACCCCAAACCGACACGGT M.tuberculosis
2179 GCAAGCGCATACACGGCCCGTACCCCAAACCAACACAGGT M.phlei
2112 GCGAGCATACTACCCCAAACCGACACAGGT M.PRIE1
2112 GCGAGCACACACACGGCCCGTACCCCAAACCGACACAGGT M.leprae
1872 GCGAGCACACACACACCGCCCAAACCGACACAGG M.gastri
1815 GCGAGCACACACACACCGACACCGACACAGGT M.kansasii
4266 GCGAGGACATACACGGCCCGTACCCCAAACCAACACAGGT M.smegmatis
                 1970
                               1980
                                            1990
                                                          2000
2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.avium
2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.paratuberc.
2908 AGGGGGACCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.tuberculosis
2298 AGGGGGACCCTACGTACCGTGAGGGCTGCTTGCGGTGGGAGC M.phlei
2231 AGGGGGGCCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.leprae
1910
                                                              M.gastri
1934 AGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.kansasii
4385 AGGGGGACCCAATGGCGTG∏AAGCC∏TTACGGCCCAAGC M.smegmatis
                 2010
                               2020
                                            2030
                                                          2040
2248 GGGATTCGGCEGCAGAAACCAGTCGGTAGCGACT-GTTTA M.avium
2248 GGGATTCGGCCGCAGAAACCAGTGGGTAGCGACT-GTTTA M.paratuberc.
2948 GGGATGCGGTCGCAGAAACCAGTGAGGAGCGACT-GTTTA M.tuberculosis
2338 GGGGTGGGTGGCAGAAACCAGTGAGGAGCGACT-GTTTA M.phlei
2271 GGGATGCGGTCGCAGAGACCAGTGAGGAGCGACT-GTTTA M.leprae
                                                              M.gastri
1974 GGGATTCGGTCGCAGAAACCAGTGAGAGCGACTTGTTTA M.kansasii
4425 GTGAGTGGCAGAAACCAGTGAGAGCGACT-GTTTA M.smegmatis
```

Figure 41

	2130	2140	2150	2160	
2367	CCGTTAACCCGT	AAGGGTGAAGC	GGDGDDTTT	DDCCCC M midus	_
2301	CCGTTAACCCGT-	-AAGGGTGAAGC	GCACAAMMM	77CCCC 14	
3007	CCGTTAACCCGG-	-AAGGGTGDDGC	<b>ここりこり 2 かかかめ</b>	77CCCC W	
2457	CCGTTAACCCTTT	GGGGGTGAAGC	GGNGNNTTT	AAGCCC M. tuber	Culosis
2390	CIGTTAACCCGA-	-AAGGGTGAAGC	GGAGAATTT	DRECCC M.pniel	•
1910	<b>G</b>		OUNGARIII.		
2094	CCGTTAACCCGG	-AAGGGTGAAGC	CCDCDDTTT	M.gastr	
4544	CCGTTAACCCCCT	COAACTOOODO	GGAGAATII. GGAGAATTTT	NAGCCC M. Kanse	ISII
		<u></u> good.on.ac	GGAGAATTT.	MGCCC M.smegn	natis
		•			
		<b>-</b>			
	2250	2260	2270	2280	
2405					
2485	GTAACGACTTCCC	ACTGTCTCAAC	Catagactc	GCGAA M.avium	ì
2485	GTAACGACTTCCC	VACTGTCTCAAC	CATAGACTC	GCGAA M.parat	uberc.
3183	GTAACGACTTCTC	ACTGTCTCAAC	CATAGACTC	GCGAA M.tuber	culosis
25//	GTAACGACTTCTC	VACTGTCTCAAC	CATAGACTC	GCGAA M.phlei	
2508	GTAACGACTTCTC	lactgtctcaac	CATAGACTC	GCGAA M.lepra	e
1910				V	
2212	GTAACGACTTCTC	ACTGTCTCAAC	CATAGACTO	GCGAA M.kansa	sii
4663	GTAACGACTTCTC	VACTGTCTCAAC	ATAGACTC	GCGAA M.smegm	atis
			_	•	
	<del></del>	· · · · · · · · · · · · · · · · · · ·	<del></del>	<del></del>	
	2370		2390	2400	
2605	GTTCGGTACGGTTT	GTGTAGGATAG	TGGGAGAC	TTGAA M. avium	
2605	GTTCGGTACGGTTT	'GTGTAGGATAG	TGGGAGAC	TTGAA M Darat	uherc
3305	GTTCGGTACGGTTT	'GTGTAGGATAG(	STGGGAGAC	GIGAA M. tuber	culosis
2697	GETCGATACGGTTT	GTGTAGGATAG	TGGGAGAC	GTGAA M phlei	
2628	<b>сттссст</b> Всссттт	GTGTAGGATAG	TGGGAGAC	GTGAD M Jenne	
1910			·	M.gastr	
2332	GTTCGGTACGGTTT	GTGTAGGATAGG	теселелс	TOTGED M KARES	_ gii
4782	<b>GTCGATACGGTT</b>	GTGTAGGATAG	TGGGAGAC	TOTGED M emean	etia
		,=,= =	JOURGAO	M. Ave in smediii	GCIB

Figure 4J

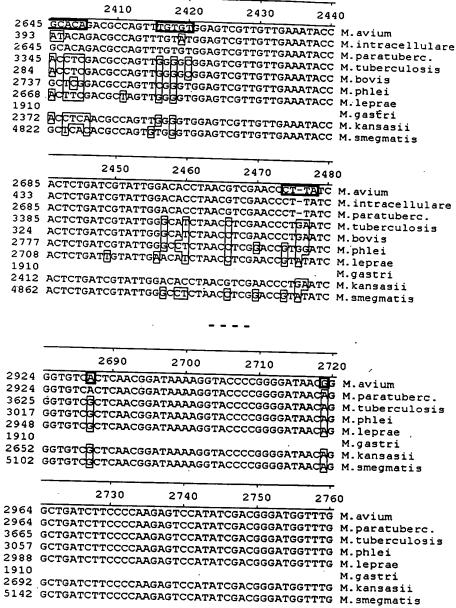


Figure 4K

```
2770
                                 2780
                                               2790
                                                              2800
 3004 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M. avium
 3004 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.paratuberc.
 3705 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.tuberculosis
 3097 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.phlei
 3028 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGAAGCA M.leprae
 1910
 2732 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.kansasii
                                                                  M.gastri
 5182 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.smegmatis
                   2810
                                 2820
                                               2830
                                                             2840
 3044 GGTCCCARAGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.avium
 3044 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.paratuberc.
3745 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.tuberculosis
3137 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.phlei
 3068 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.leprae
 1910
2772 GGTCCCAAGGGTTGGGCTGTTCGCCC_ATTAAAGCGGCAC M.kansasii
 5222 GGTCCCAAGGGTTGGGCTGTTCGCCCCATTAAAGCGGCAC M.smegmatis
                  3050
                                3060
                                             3070
                                                           3080
3283 CAAGATCAGGTTT-CTCACCOTTTTAGAEGGATAAGGCCC M. avium
638 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGGATAAGGCCC M.intracellulare
3283 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGGATAAGGCCC M.paratuberc.
3984 CAAGATCAGGTTT-CTCACCCACTTGGTGGGATAAGGCCC M.tuberculosis
570 CAAGATCAGGTTT-CTCACCCACTTGGTGGGATAAGGCCC M.bovis
3376 CAAGACCAGGGTT-CTCACCCTGTAGGAGGGATAAGGCCC M.phlei
                                                               M.leprae
1910
                                                               M.gastri
3011 CAAGATCAGGCTT-CTCACCCACTTGGGGGGGATAAGGCCC M.kansasii
5462 CAAGAGCAGGCTT-CTCACCCTGTAGGAGGGGATAAGGCCC M.smegmatis
                               3100
                                             3110
3322 CCCGC-AGACCACGGGATTGATAGGCDAGACCTGGAAGCT M.avium
677 CCCGC-AGACCACGGGITDGATAGGCCAGACCTGGAAGCT M.intracellulare
3322 CCCGC-AGAICACGGGATTGATAGGCCAGACCTGGAAGCT M.paratuberc.
4023 CCCGC-AGAICACGGGITCAATAGGICAGACCTGGAAGCT M.tuberculosis
609 CCCGC-AGAICACGGGITCAATAGGICAGACCTGGAAGCT M.bovis
3415 CCCGC-AGACCACGGGATGGATAGAICCAGACCTGGAAGCT M.phlei
                                                               M.leprae
1910
3050 CCCGC-AGAACACGGGTTGGATAGGCCAGACCTGGAAGCT M.kansasii
5501 CCCGC-AGACCACGGGATTGATAGACCAGACCTGGAAGC M.smegmatis
```

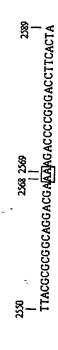
Figure 4L

	1	.30	140	150	160
	_				160 
107	GAGTAACAC	GTGGG <u>CA</u> AT	CTGCCCTGC	ACTTC-GGGAT	AA M.avium
59	GAGTAACAC	GTGGGCAAT	CTGCCCTGC	ACTTC-GGGAT	AA M.intracellulare
107	GAGTAACAC	GTGGGCAAT	CTACCTGC	ACTTC-GGGAT	AA M.paratuberc.
70 70	GAGTAACAC	GTGGGCAAT	CTGCCCTGC	ACTTC-GGGAT	AA M.scrofulaceum
209	GAGTAACAC	GIGGGIGAI	CTGCCCTGC	ACTTC-GGGAT	AA M.tuberculosis
120	GAGTAACAC	GTGGGTGAT	CTGCCCTGC	ACTTC-GGGAT	AA M.bovis
69	GAGTAACAC	GTGGG[[AA1	CTGCCCTGC	ACTTOMGGGAT	AA M.leprae
70	GAGTAACAC	GTGGGCAAT	CTGCCCTGC	ACACC-GGGAT	AA M.kansasii
104	GAGTAACAC	CTGGGCAA1	CTGCCCTGC	ACACC-GGGAT	AA M.gastri
64	GAGTAACAC	GTGGGGAAT	CTGCCCTGC	ACMTC-GGGAT	AA M.gordonae AA M.marinum
04	GAGTAACAC	GIGGGCBAI	CTGCCCTGC.	ACTTC-GGGAT	AA M.marinum
		•			
				•	
					<u> </u>
	4	50	460	470	480
424	D D D C C M C M M	TON CONTROL	n con nooma	cccdmmmmnmc	CGG M.avium
376					GG M.intracellulare
424					GG M.Intracellulare
387	DANCCICII	TCACCATCG	ACGAAGGTC		GG M.scrofulaceum
389	AAACCICII	TCACCATC	ACGARGET	CCCCENTORCEC	GG M.tuberculosis
528	ABACCTCTT	TCACCATC	PACCARGOTO	CGGGTTCTCTC	CG M boyis
439	ADACCICII	TCACCATC	PLCGARGGIC	Mccch Arrer	GG M.leprae
386	ABACCTCTT	TCACCATCC	PLCGANGGIC	CGGGLALICIO	GG M.kansasii
387	AAACCTCTT	TCACCATC	DCGAAGGTC	CGGGTTCTCTC	GG M.gastri
420	ABACCTCTT	TORCORTO	BCGAAGGTC	CGGGT1201CTC	GG M.gordonae
381					GG M.marinum
301	AACCICI	TONOCATO	ACOMMOOTE	00001111010	og m.marmam
	- 4	^ _	500	510	520
	-			7.7.	777
429					TG M.tuberculosis
568					TG M.bovis
464	ATTGACGGT:	AGGTGGAGA	AGAAGCACC	GGCCAACTAC	TG M.avium
416	ATTGACGGT:	AGGTGGAGA	agaagcac <u>c</u>	GGCCAACTAC	TG M.intracellulare
464	ATTGACGGT.	AGGTGGAGA	agaagcac <u>-</u>	ACTAC	TG M.paratuberc.
424	GTTGACGGT	AGGTGGAGA	AGAAGCACC	GGCCAACTAC	STG M.scrofulaceum
479					TG M.leprae
426					GTG M.kansasii
427					BTG M.gastri
460	GCTGACGGT	AGGTGGAGA	AGAAGCACC	GGCCAACTAC	GTG M.gordonae
421	ATTGACGGT	AGGTGGAGA	AGAAGCACC	GGCCAACTAC	GTG M.marinum

# Figure 5A

						•
		1130	1140	1150	110	50
1104	TCTCAT	STTGCCAG	GGGTAATGC	GGGGACTCG	TCDCDC	<b>M</b>
1098	TCTCAT	STTGCCAG	CGGGTAATGC	GGGGACTCG	TCDCDC	M.intracellulare M.paratuberc.
	TOTOMIC	7 I I I I I I I I I I I I I I I I I I I	CHITTTENTOTOT	~~~~~~~~		_
~~~	TOTOMIC	TIGULAG	CHHISTAATCCC	CCCCTCMCA		
	- LOLONIC	TA LUCLAR	しほぼばずりりずにここ	CCCC30maa		
-100	ICICAL	JAJJULTAG	CGGGTDDTGCC	GGGGTCMCC	2222	
1061	TCTCATO	TTGCCAG	CACGTAATGGT	GGGGACTCG:	TGAGAG	M.gordonae
			46.20 1 W. 1 GB I	GGGGACTCG.	rgagag	M.marinum
						•
		1290	1300	1210		_
1264				1310	132	0
1264	CGAATQ	TTTTPAA	GCCGGACTCAG	TTCGGATTGG	GGTCT	M.avium
1210	CGAAICC	TITIAAA	*CCGCMCTCNC			
1224	CGAATCC	TTTTAAA	3CCGGTCTCAG1	TCGGATOGG	GGTCT	M.paratuberc. M.scrofulaceum
1229	CGAATCC	TTA-AAA	SCCGGTCTCAG	TCGGATCGG	GGTCT	M. tuberculosis
1368	CGAATCC	TTA-AAA	SCCGGTCTCAG	TCGGATCGG	GGTCT	M. bovis
1279	CGAATCC	TTTTAAA	SCCGGTCTCAGT	TCGGATCGG	GGTCT	M.leprae
1226	CGAATCC	TTTTAAA	SCCGGTCTCAG	TCGGATCGG	GGTCT	M. scrofulaceum M. tuberculosis M. bovis M. leprae M. kansasii
1227	CGAATCC	TTTTAAA	SCCGGTCTCAGT	TCGGATCGG	GGTCT	M.gastri
1260	CGAATCC	TTT <u>T</u> AAAC	SCCGGTCTCAGT	TCGGATCGG	GGTCT	M.gordonae
1221	CGAATCC	TTT <del>[</del> AAA0	CCGGTCTCAGT	TCGGATCGG	GGTCT	M.marinum
			_	J		
						•
		1330	1340	1350	136	,
1304	GCAACTC	TA CCCCTA				
1256	GCD DCEC	SACCOMI	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.avium
1200	CCARCIC	ACCCCA1	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.intracellulare
1250	GCAACTH	ACCCAAT	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.paratuberc.
1269	GCAACTC	ACCCCGI	'GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.scrofulaceum
1407	GCAACTC	ACCCCGI	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.tuberculosis
1401	GCAACTC	PACCCCCTI	'GAAGTCGGAGT	CGCTAGTAA	TCGCA	M hovie
1266	CCAACTC	ACCCCGI	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.leprae
12,00	GCMMC I C	- WOOCOURT	GAAG I CGGAGT	CGCTAGTAA	TCGCD	M kangagii
1207	GCAACTC	ACCCCGI	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.gastri
1300	GCAACTC	ACCCCGI	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.gordonae
1260	GCAACTC	FACCCCET	GAAGTCGGAGT	CGCTAGTAA	TCGCA	M.marinum

# Figure 5B



Mavium 23

Figure 6

491    GTAG	
<i>473 414  471</i>  -	883   TGACGGGGC
41 42 42 493 49       1       IGGAGAAGAAGGACCGGCCAACTACGTGCCAA <mark>CA</mark> GCGGCGAATACGTAG	43   11   GTACGGCCGCAAGGCTAAAACT <u>LA</u> AAGGAATTGACGGGGG
452      GAAGAAG©AC	GGCCGCAAGG
41 	843      GTAC

M. tuberculosis 165

Figure 7